

0015001300

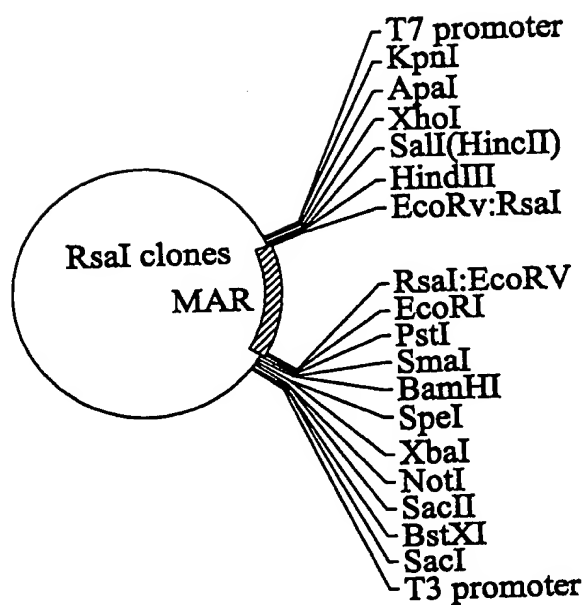


FIG. 1A.

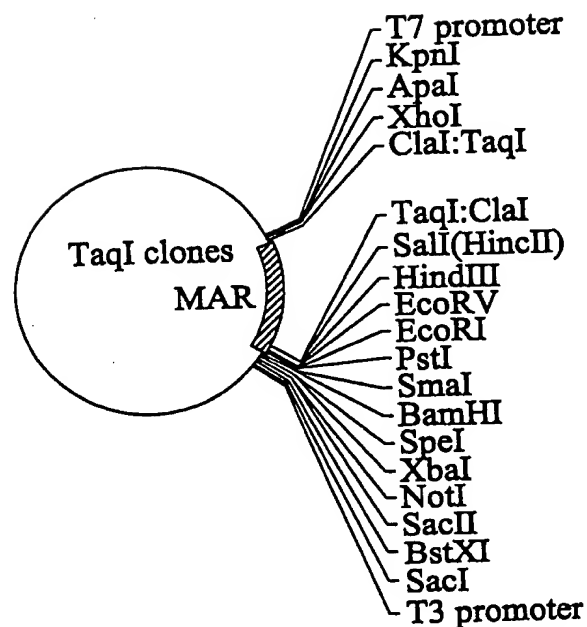


FIG. 1B.

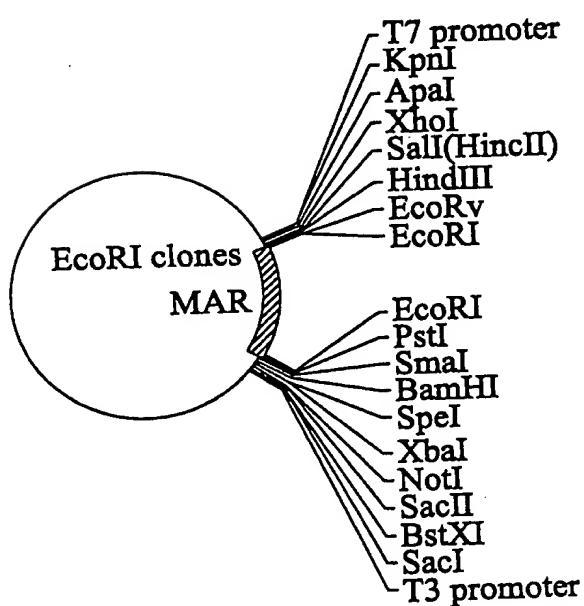


FIG. 1C.

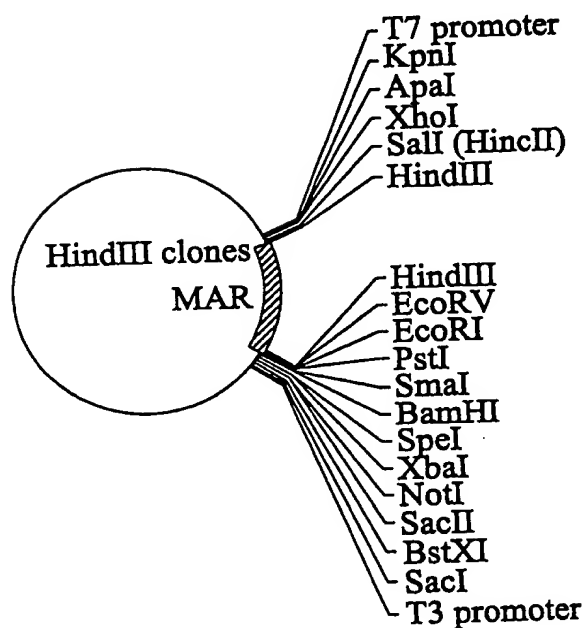


FIG. 1D.

**FIG. 1E.**

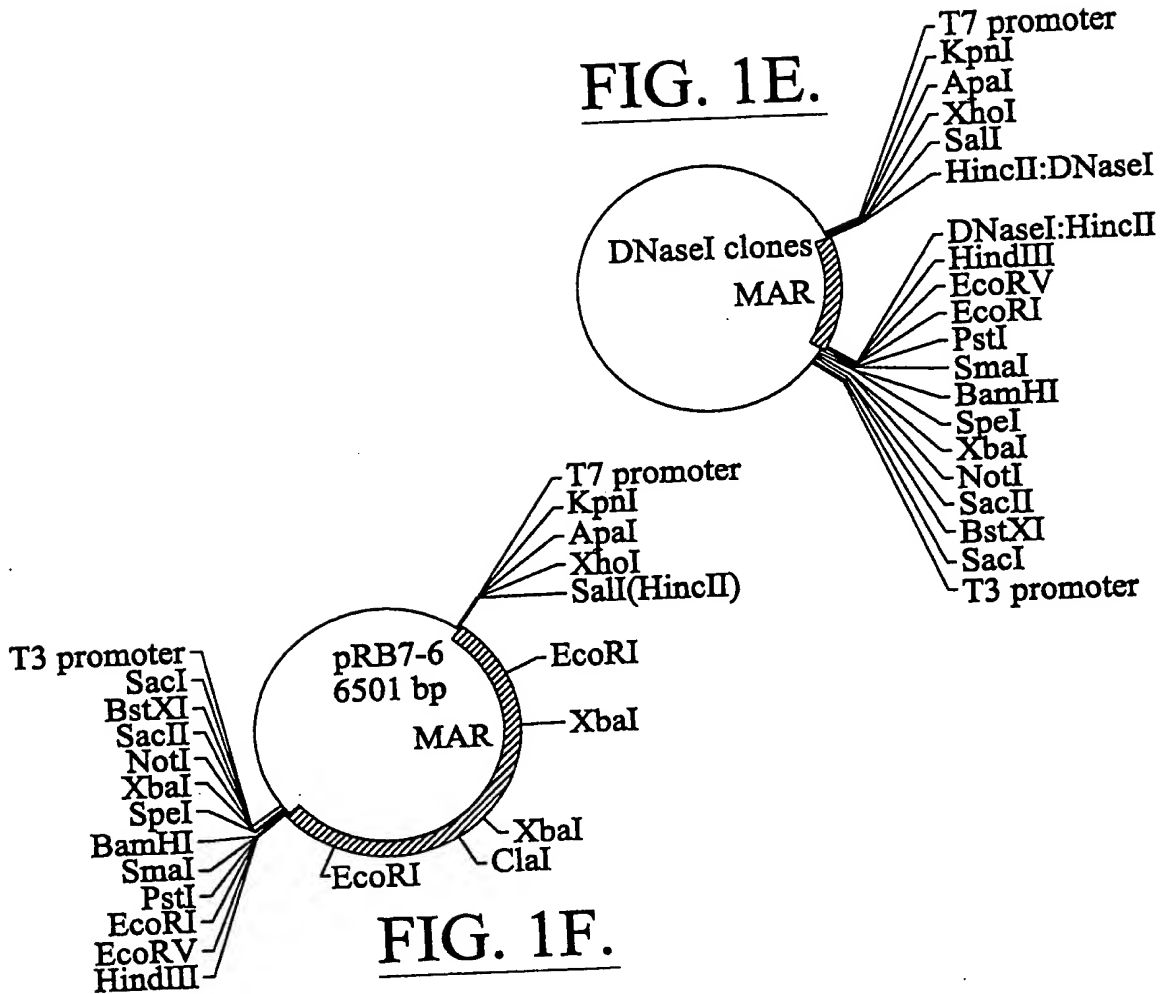


FIG. 2A.

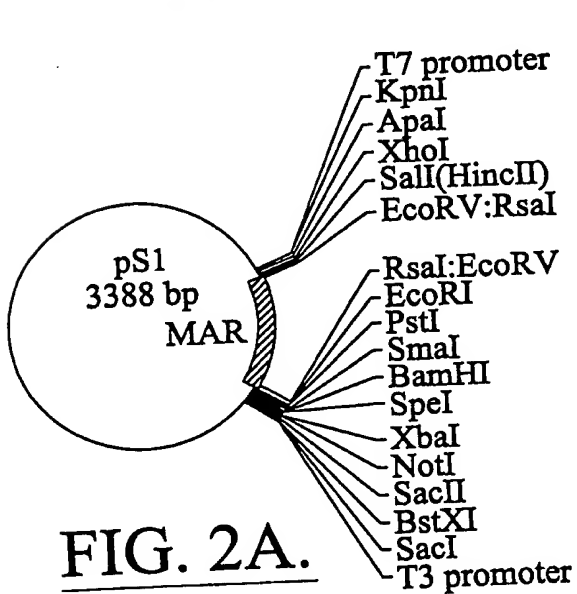


FIG. 2B.

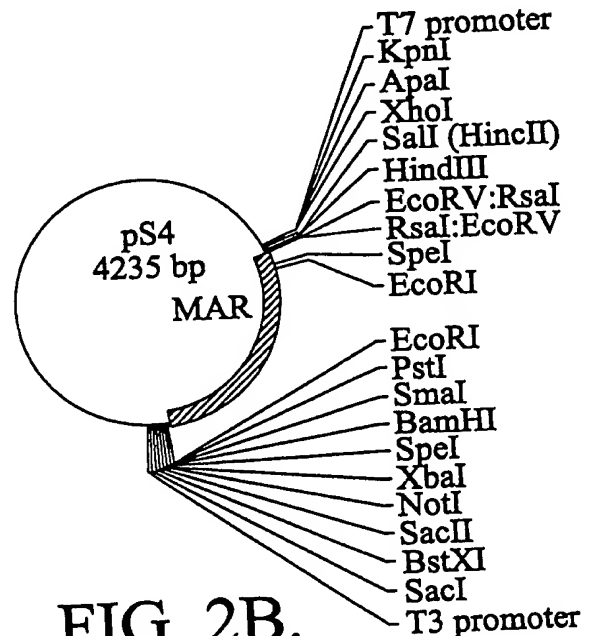




FIG. 2G.

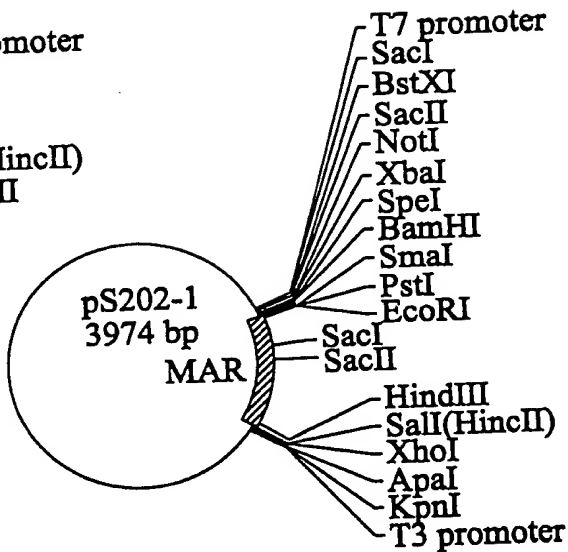
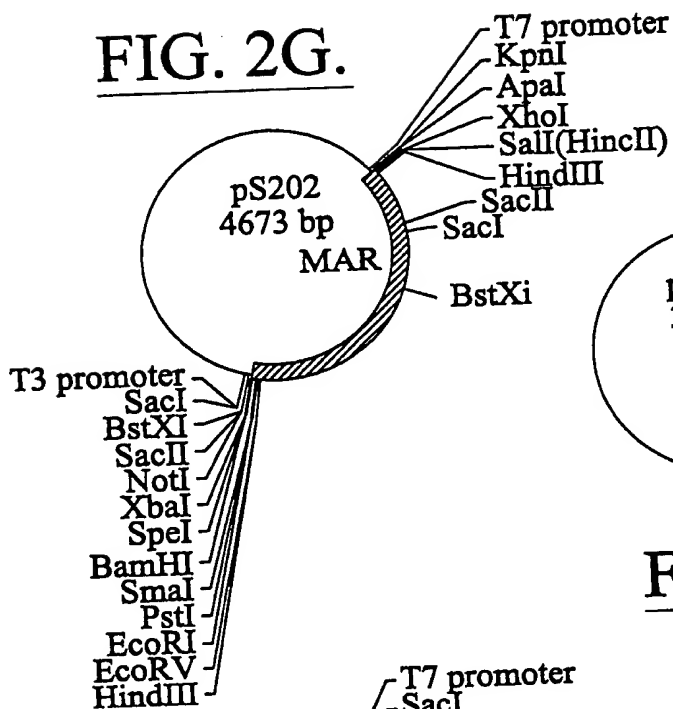


FIG. 2H.

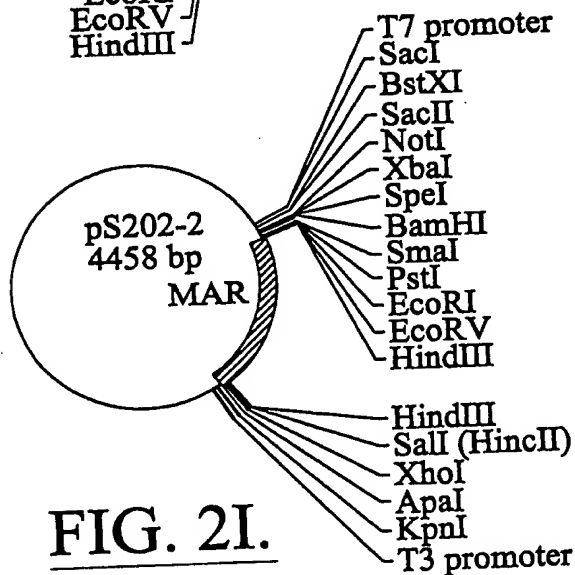


FIG. 2I.

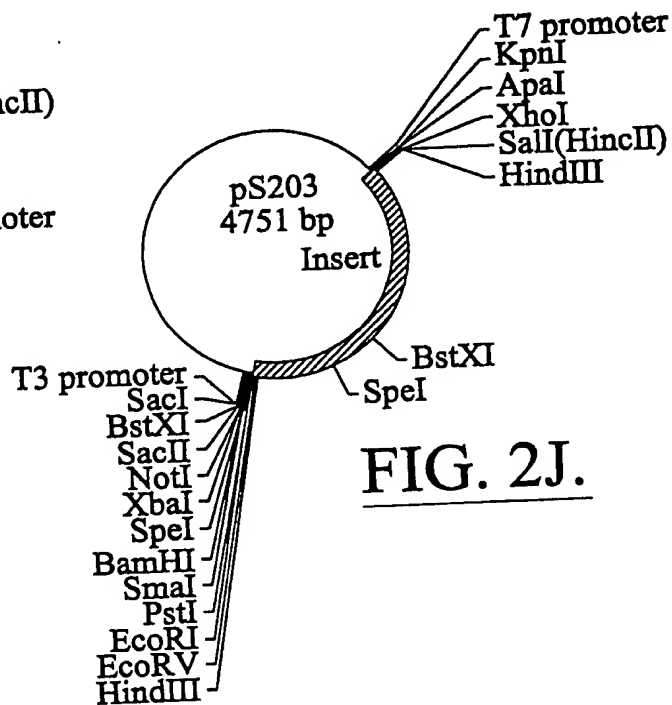


FIG. 2J.

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FIG. 2K.

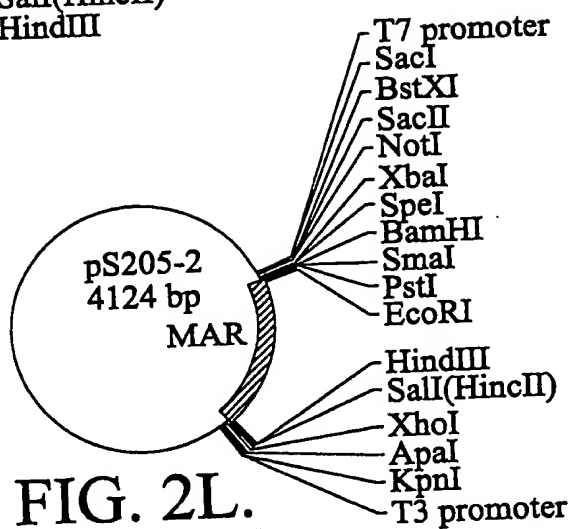
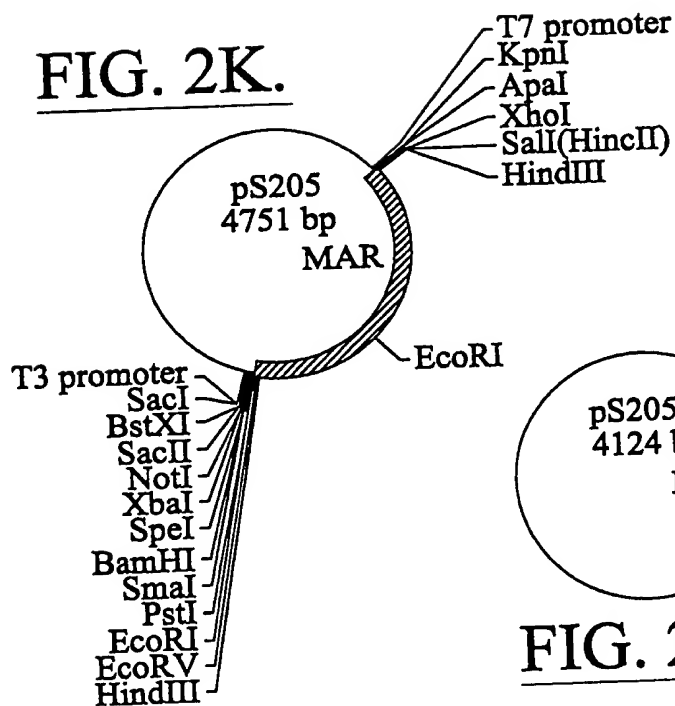


FIG. 2L.

FIG. 2M.

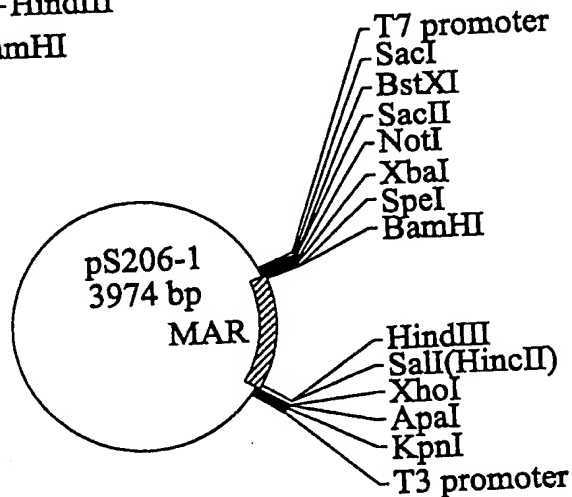
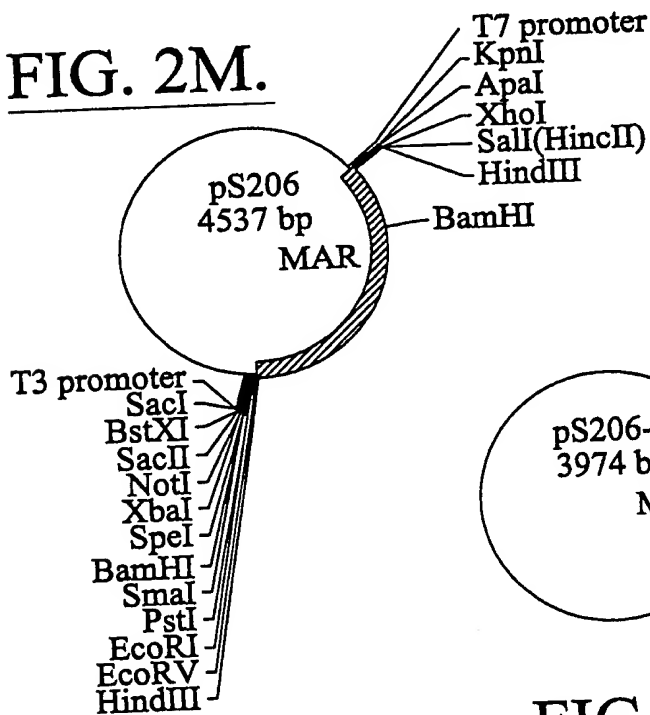
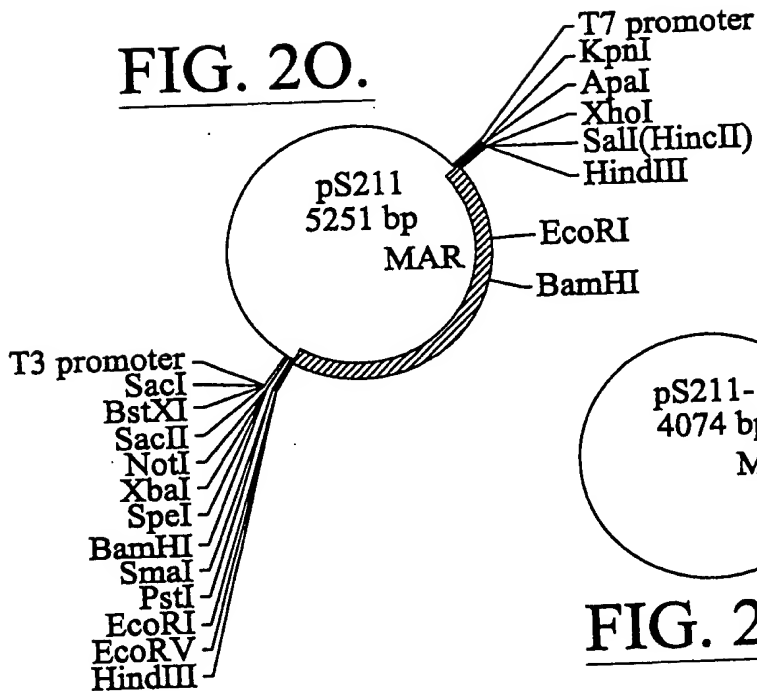
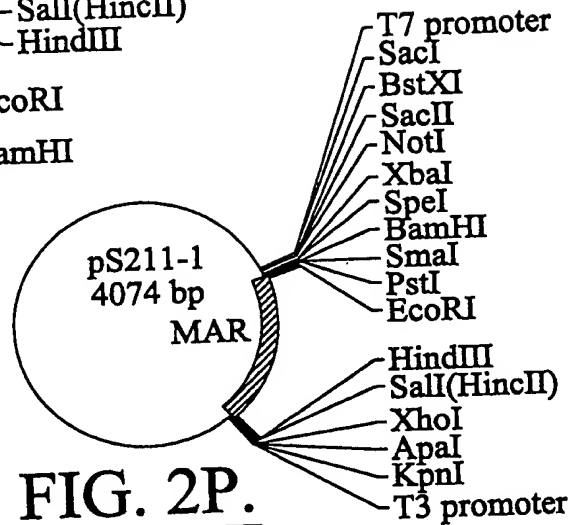


FIG. 2N.

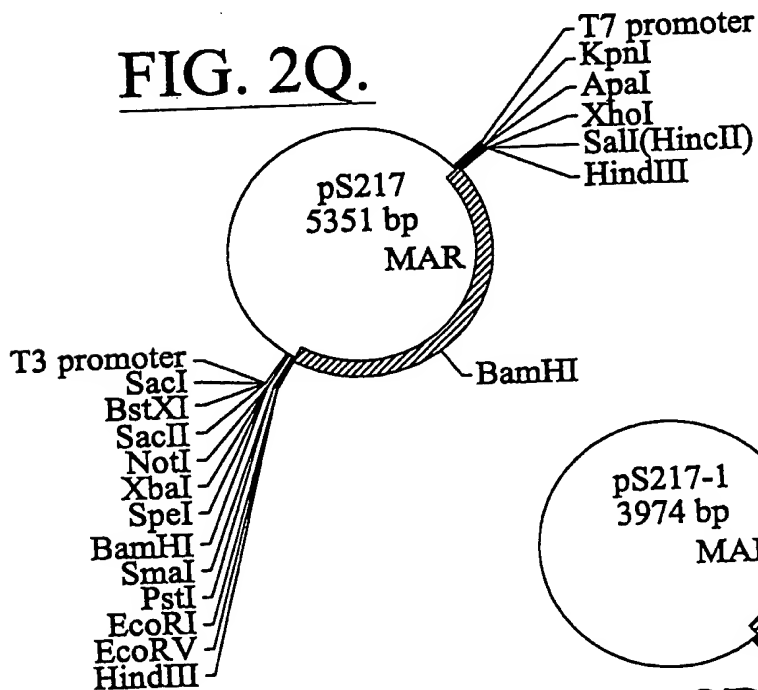
**FIG. 2O.**



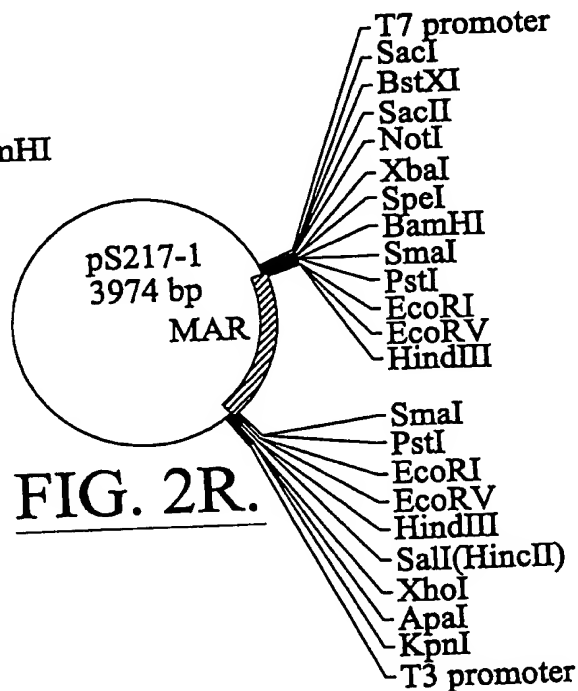
**FIG. 2P.**



**FIG. 2Q.**

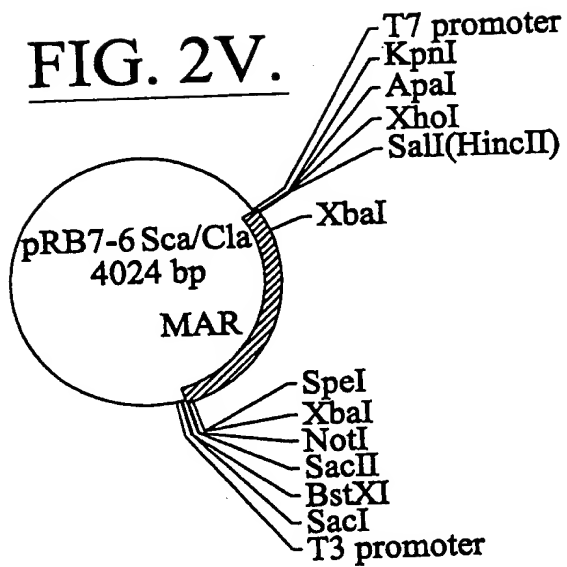


**FIG. 2R.**

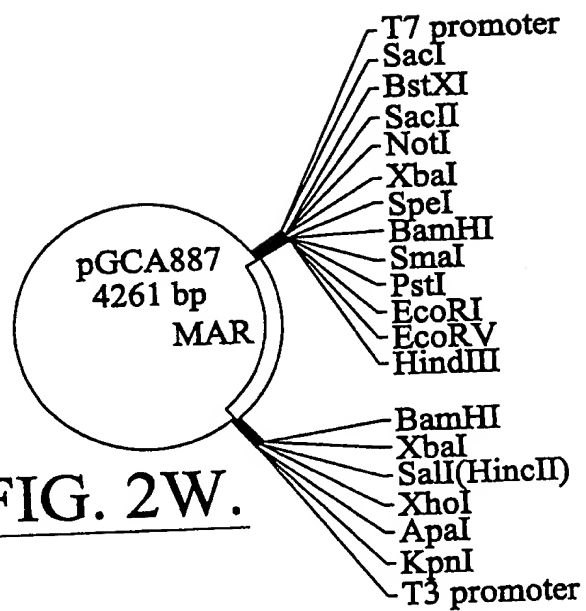




**FIG. 2V.**



**FIG. 2W.**





pS1 (SEQ ID NO:1)

1 GATACGTAAA CAACGTGTAT CCAGTAAGTA TCAAGCCTAA TCTCGAAGTG  
51 GTAGAGACGA GATGACCGAC TTTGACACTC ACTATGGGTC AATAATAATA  
101 ACTGAAATAA AACTAAGATA TTTAAACCAA CATGATTTAC AGAATTTACA  
151 ATAATTTATT TAATCAGCAG AAATAATCAA ATTTCTTCAA ATGTAACAAT  
201 TCTCAATATA TTAATTAAAT TCCTTCAATT CAAATAATTT CTAATTTATC  
251 AATTAAACCT CATTTACAGG AGTAACAATT AATTCCTTAA CAAGCAAGAA  
301 TAATAATTCA TTAAATTCCA AGGATTTTTC AATTTATTAA TTAGCTTCAC  
351 AACCTGAAAT AAATTATTAA AGTATCGTGT AATTATTATT ATTAAGCACG  
401 ATTTCTGCCG AGGACATACG GCCCGATCCA GAGTATC

pS4 (SEQ ID NO:2)

1 GATACTAGAG TGGTGTATC AATTCCTACT CGTATGAATT AATTAAATTT  
51 GTCTCTTATT TCTGTCCTAA GTCATATACA AGAAATGCTA ACTCCATCCG  
101 TTTCAATCCC TATGACATAG TTTGATTTGA TTGAATTTGA AAATTTAAGA  
151 AACAAAAGAT AATTTTTGTG ACTCATAATT TAGACATGTG TTATAAGACT  
201 TTTCTCATGA ATTTTTTAGA AACAAATGAT AATTTTTGGA ACTCATAATT  
251 TAGACGTTTT ATAAAAATA CTAAGTGCAT CTGGTTCAAT ATTTATGTGT  
301 TATTCCTATA AAAGTTCTGG ACTTATATTT TTAAATATTT CATAATATTT  
351 GGTATCGGTA TAATTTTTTT GTCACTTTTG GATGAAAGGG AAGTTTAAGT  
401 AAATTTCTTT TTCCAAATTT AGAAAGTTAT AATATTCTTT TTAACGCG  
451 CAAAAAGAAA AATAAGCTAT TGATTATTAT AAGCCTAAAC CAAAAGAATT  
501 CTTTGACTAG TAGGAAGCCA TTTTAAAGTT AGGCGCCAAA ATTCAAAGCC  
551 AACGTGGGCA TATCTCCAAA CTGGCGGCTA CAGTATC

pS8 (SEQ ID NO:3)

1 ACCGCTTTTA TTATTATTAT TTTTACCGAG AATTACAACA TCATGAAAAT  
51 ACATCTCGAA CCACGTCACA TCAATGCACC CGCGGTTATT GACATATTTT  
101 AACTCTGTTG AGATTTGGAT TTGGGTCACA TAAATGTGCA CCCGAGTTTA  
151 AGAGGATAAC ATTATTAAAT ACGCGCCTAA AACGACTAGC GTATCATTAT  
201 TTTGGGTAGG GCCGTGAAAT TTTGCTAAAC TGCCCATCCA GAAATCTAAG  
251 TAATTTTACC AACACGTATA GAGGGCCCCA CAGCTTGTGT ATTTTGTGTT  
301 GTCGAGGCTC GTCTCATTCA TTATTTTAA AAGGAATTTG CAACGTCGTG  
351 GAAATGCATC TCGAACCACG TCACAATCAA TGA

FIG. 3.

pS115 (SEQ ID NO:4)

1 GAATTCGATA GACTCACTTA AATATTAGAA GTGAATTACC TAGAGTTAGA  
 51 TCCAAAACAA TTATCTTGCA CCTATCCTAT CAACCCTTAT CTTTCCCAT  
 101 TGATTACTAC CTTGCTTACC TTTGTTACGA TTTTCATTAG ACAATAACTT  
 151 TAGATTCTTA GTTAATTGCA GTTAGAAATT ATATTAAATT TCAATTGTTG  
 201 GATCATCTTG AATACCAATC AAGCTAGAAA ATACAAGAAT ACTGTTTAAA  
 251 TCAAATCCAT GTGGATACGA TATTATACTA TATTATATTT GACTTGTGAG  
 301 CATTATTTAT GTGTGTTTTG TGCTCGTCAA AGTTTGGCGT CGTTGCCGAG  
 351 GATTGGCAAT CAATAGTGT TGAAATAGTT TTTGGTGCTA ATTTAGGAAT  
 401 TAGGTTTTAT TTATTTATTT TTTCTTTTCT TTTCTTTTCT CTTTCTATT  
 451 TTATTTCTT TATTAGTTAA CTTCTTTTCA AGATTTTTTT TGTAGTACCT  
 501 AACAAGTTAG AGAAGATACT GTAGATTTTG AACTCTAAAT GTTGGAAGA  
 551 TGGAGTACAA CCAGCCTAAG AAAATATTTG AATAGTTAGC AGCTGAACAT  
 601 TATCGGCGGT CGGTTATGCG GTTTAAATGC GGTGGAAGCA TCTACCACCG  
 651 CAGCCTAAAG AAAATATTTT GAATAGTTAG CAGCTTGAAC ATTATCGGCG  
 701 GTCGGTTATG TGTTTTAAAT GCGGTGGAAA TCATCTACGG GCTAACTGTC  
 751 AAGCAGGTAT GTATTCTTCC TATGGTTCGT ATTTTGAGGA GTCTACTCT  
 801 GTTTCTAGTT CGTACATGTA TGAGGATTCA TATGGGCACA ACTCTGACTC  
 851 TGGTTGGGAT GAATTC

pS116-1.1B (SEQ ID NO:5)

1 GAATTGTATT ATTGTTAGGT GGGAGAGATT TTTGACTATA TGGGTAAAA  
 51 TCAGCGACAA AGGGCCAAAT ATACCTATTT ACTTTTAAAA ATAGTCTAAT  
 101 AATACCTCTC GTTATATTAT TAGGTTATCT ATACCTTTCG AGTCATATTT  
 151 TGGGTTCAAA TATACCCCTC ATTTAAACGG AGGGACACGT GTCATCGTCC  
 201 TGTTGGTCAA TTCTAAATAT CTCCTAATTA ATTA AAAAGA CTCATTACCC  
 251 ATATCCGAAA AATATTTTTT AAAGCAATAT TTTTTTATAA AAAATGGAAA  
 301 AACTGAAATT ATTTTTACTA AAAATTGAAA AAAACGAAAA TAGTTTTTTT  
 351 TCAGTTTTTA CAAAAAACT ATTTTAGAAA AAATTGAAAA ATATTTTCTA  
 401 AAACAATGTT TTTGTAAAAA CTGAAAAAAA AGAAGCTGAA AATCAATTTT  
 451 CTAAAGCAAT TTTATTTGTA AAATCTGGAA AAAACTACTA AAAACTGAAA  
 501 AAATGAAAA ATTTTTTTT CTAATTTTTA CAAAAAAAC TGCTTTAAAA  
 551 AAAGCTGAAA ATATTTTCTA AAACAATATT TTTGTAAAA CTAAAAAAA  
 601 AATATTTTCT TCTTTTTTTC AGTTTTTAGT TAAAAATATT TAAGTTTTTT  
 651 CCAGTTTTTA ATTACTTTAG AAAATTACTT TTCTGCTTTT TTTTCAGTTT  
 701 TTACAAAAAT ATTATTTTAG AAAATATTTT TCAGTTCCTT AAAGCAGTTT  
 751 TTTTTTGTA AACTTGAAA AACAATATTT TCGTTTTTTT CAGTTTTTAG  
 801 TAAAAATTTG TTTTAGTTTT TTTTCAGTTT TACCAAAAAT AAAATTGCTT  
 851 TAGAAAAATTA TTTTTCGGGT ATGGGTAATG GGTCTTTT ATTAATTAGG  
 901 AGATATTTTG AATTGATCAA TAGGACGATG ACACATGTCC CTCCGTTTAA  
 951 ATGAGGTGTA TATTTGAATC CAAAGTAAGA CTGCAGCCCG GGGGATCC

FIG. 3. (continued)

pS202-1 (SEQ ID NO:6)

1 GAATTCGATA TGGCTTGTG GACAAGAATT AATGAATCAA TTGTGAAAA  
 51 GTTGATGGAC ATATTGAAGG TAAATCATA TACTATTTT CTAAATCTC  
 101 TTTTAAATGT TCCCAATTA TCTGATTCT ATATTGCTCT TAAATGTCAC  
 151 TCAACCTTAG ATCAACAAAC ATATAACTTA CCCAGTACAT AAGAGATTGC  
 201 GGCATTATGG CTTGAAGAAA ATCCTAGAGA CACATCTGCA CCACATATT  
 251 GAATTTATAC CCACAGTAAT AGAGCTCGGT TAGTACATTA TTATTATGGA  
 301 TGTTACGATC CGTTGCAGTA TCCATTATTA TTTTCCTTCG GTGAAAATGG  
 351 ATGACATTGT GGAATTAATA AAATTATTCA GACAAAAAAT TCGACGAAAC  
 401 GTAGAGCTTA CTGCGAACAT GAACAATTGC CCAGTATATC AAATACGTGT  
 451 TCAGTTGATG GATTCCTTGA TATGGAAGAT GAATCACTAC AAAGAGGAAA  
 501 ACGAAAAAGA GATACAGTGT CTTGTCGAGA GTATTATTGT TACAAATTTC  
 551 AACTAAGAAA TAATGAAACA AATGAAGTGT TACATTGTGG GAGAATATTC  
 601 CAACAATTTA TAGTAGATAT ATATATATAA AGCTT

pS202-2 (SEQ ID NO:7)

1 AAGCTTGCAC GCCTACATCG TGGGATAATT TAGAAAAAGG AAAGGGTATA  
 51 TTGGATCCCC CTATCATTG TGAAACAGGT AACCATACGA GAACCCCTTT  
 101 CGCTTCCTGA AAAATGTTAT ATATTGTTGT ACTCATATT ATACACTATT  
 151 TATTATTAAT ATAACGATGC TTATTTTGT TGGAGATTGG AGATTATCAC  
 201 AGCTTATTTA TCTTATATTG TATCTTATTA AACTTAAAAA CATAAATACT  
 251 ACGTGCTCTT TTAATTTGGG ATCTATTAAG GGTTCGTTGC ACGCTTTTAA  
 301 ACATCTTGGC TATTCTGTTT ACCAGCTGCT ACCTTAGCCT GTATGCTTAC  
 351 ATCATCTCCT AATTTAGACA AAGGAAAGGG TATATTGGAC CCCCCTATC  
 401 ATTCTGTAAA CAGGTAAACA TACATTCAGA TTATACTCTT TTCAGAATGA  
 451 CATATTGTTT ATACATTACT GTAAATTGTG ACTATTTGTA TATTAGGGTC  
 501 CACATCGGGT ACATCTAACC TGCATCATGT TATCTTGAAC ACTGTTCCAA  
 551 TCAAAGGTTT GCACAAACTT AATGTTACAA TCATGTCCAC CATACGTATG  
 601 CCTTGGTGCT CTTTTTTTTC CTAATGATAC TTCTTATATA TTCAGTCAT  
 651 AGGCGGGCCA GAAAGGTGTG CCTGGTCACT AAAGAGCAAC GAAGTGAGTA  
 701 TGTTGCTCTA AAAAGGGTCC CACACTGTCA ATTCTGTCAT CCAAAGAAGT  
 751 TTGAATATGA ACCTCCAGGA TTTTGCTGTA ACAGTGGTTC AATAAGGTTG  
 801 ACATCTCATA AAATGCCAAC TGAATTATCG GAGTTATACT TTGGAAATAC  
 851 TGAAGAATCT GAAAATTTTC GAACTTATAT TAGAACATAC AATAACATGT  
 901 TTGCATTTAC TTCATTGGT GTCAAGTATG ATAAAGAGCT AGCGAGAAGA  
 951 AATTGTGGTA TCTACACATT TAGAGTCCAG GGACAGATGT ATCATTTTAT  
 1001 AGATGATTTA GTTCCTTCCA ATGAAAAACC TAGGAATTTA TAGCTGTACT  
 1051 TCTACGATAA TGATAATGAA CTAGCCAAAT CAAGCTT

FIG. 3. (continued)

pS205-2 (SEQ ID NO:8)

1 GAATTCTTCA GCCATTGTAC ATATAGTTGT GTATTAATGT TATTAATAAT  
51 GGATAATTAA ATATATACCT GGAATAAATA TACGATATTA TAATAGTGTG  
101 TAATTATATA TAAAAATTAT ACATAATATA ATGATGGTAT TTAATATAGC  
151 ATAAATTTGA ACGATCTGGA TTGATTTCTT GAATCAAAAT AGAGTTGTGT  
201 GAAAAGAAAA GAATGAGATG AAAAGCAAAG TATGAAGAGA TGAATTTGTG  
251 TTTTTTTTAT GGAGGAGGAA GGTTCCTCAGT GATGGAATCA TCCCTGGTTT  
301 TCTTTAGCAC CAATGAAAGT AATGAACCCC CCCCCAAAAA AAAAAAAAAA  
351 AAAAAAAGG GAGAGAGAGT AGAATGGAAC GGCTAGGTGA AAGTATAGGA  
401 GTAGAAATTA GGTTCAGGGA GAGAAAAGGG GGGAAATTAA TTCCTAAATT  
451 AATGGGATTC TAATTTTTAA ACTGTTTTGA AATATTTTAA AAGTAGTGTT  
501 ATTTATATTA TTAACTTTTA AAAAAAGTCA AACGAGGTAA AAATCCCATG  
551 GGGGAAAATT TAAATGGTTA GTCTTCTATA ATATTTTCAA CTCTGCTTAG  
601 CACTAAAAAT TAGTCTAAAA ATAACCCTAA ATTAGTGTAT CTAAATTAAT  
651 TAGTTCATCG AACAGGAGCA TTGGATTATC CCTCCAGAGT TACACAGGAA  
701 GCTT

pS206-1 (SEQ ID NO:9)

1 GGATCCAGCT ATTATTATAG CATGTGAGTT GTCCGTGAAC AGCTAATTTT  
51 TTACCACACC CAAATTCAAT ACTATTTTAG TGTAATATA TCTTTTAGGT  
101 CTAGTCTTAA TATTTAACTT TTTGTCTTAC TTTTAATAGA TTTTATTTGA  
151 GAAAAATTAA TAATTACAAA AAATAAAAAAG TATATATTCA CATACTTATA  
201 GTACAACTT TGTCTTATT TATAAAGAGA AAAAGAAATT TTACAAAAAA  
251 CAAATATATT TGCTTTCTTT TAATTAGTAG TTTTATTAAG CAAGCTATAG  
301 AAGCTC

pS211-1 (SEQ ID NO:10)

1 GAATTCCTGT GTTTGTAGCAC GGTCGCTCAA TTGTCATATT TGGCTCATTT  
51 ATCTGATTTT TAAACAATTA AGAACTTATA TGCAAATTTA ACTTTTAAAA  
101 CCGCTTTTAT CATTATTTAT TTTATACAAA ATTACAACGT CGTGAAAAGG  
151 CATCTCGAAC CACGCCACAA CCAGTGCACA CGTGATTTGT TGACGCATTT  
201 TGGACTTCGT CAAGATCGTG ATTTGGGTGA CATAAATGTA CACCCCGTAT  
251 TTAAGAAAAAT AACCTTATTA AATATTGCGC CAAAATACTA CGCGTTATGA  
301 TACTATTAGG GTAGGCTTGT GAATTTTACT AAATCGCCCA TCTCGGAATC  
351 TAGGTATTTT CTTATATTAA AAAAAATAAG ATGGGGGCCT GCAATTTTTT  
401 ATTATTTAAT ATTTATTTAT TTTTGTAGCGA AGATCCCTCC CTTATTTTAT  
451 GAATACCCTT TAATGACTAC ATCTTTATTA TTAATAAGTT TGTCTATAAT  
501 TATGAAGTCA ATCTCTACAT ACATAAAAAAT AACATATTAA TTAATAATTT  
551 AAAACAAATA TTAATGGAAA GTAATATTAC TAAAATTATA ATTACAAACA  
601 ACATGGAATT GTCACAAAAAT AAAAAATAAA AACTAATTAT CCCATAGTTG  
651 GATTAAAATT CATATTGTGA GTATGACTTA AGCTT

FIG. 3. (continued)

pS217-1 (SEQ ID NO:11)

1 AAGCTTTAAA AGGAAGAGAG CCACAATTTT CTTTGACCTT CCTTCTCTCC  
 51 TAGCCACTAA GATATACAGT ACTGGTCAAA AAGAGCATAT TTATAGCTCA  
 101 AAATTTTGCC TTTTCTGTT GTAAACGTGA TTGTTTCTTA CTTGGATTCT  
 151 TGTCTATAT ATTTACGGGA GAAAAGAGCA ATTTGCATGC TCCTAAATCT  
 201 TTTATTTTCT GGTGAAAAAT TGGTCTTTAA TTGGCTGGGA ATTATTTTTT  
 251 AGATGCTACA ACCTTGACAA ACACCTAAGA ATATTTTAGT GACAATGGCT  
 301 TGTCTTTGA GTACTGGTTT TTCTGTTTCT GGTCCCTGTT TCAACGCCAC  
 351 AGCCAAAGAG TCTCGTCGTC ATTGCCCTTC GATTGGCACT CTGCAACTTA  
 401 AAGATTTAGC ATCCAGAGAA TTTCTAGGCA AACCCTTGGA TTATGCATCA  
 451 GATCATATTG GACTAACCA TTGGAATGTT GAACGACTTT CTGTATGTAA  
 501 ATCTCTGATA CATTTGCTTC TGTGTTTATA CTTGGTGTTT TCATGTTTTT  
 551 ATTCTTGTTT TAAATTTTTT GAGATCAAAT CATTTATAAG TATTTATTCT  
 601 AATGATTTTA GGCACAAGTA TCAATCGCTG CTCAGAGATG GTGGGAGAAG  
 651 ACCCTTAAAC CCAACATGGT AGAGATCAAT TCAGCAACAC AACTTGTTGA  
 701 TTCATTATTA AAAGCTGGTA ATAGATTGGT CATAATTGAC TTCTTCTCTC  
 751 CTAGCTGTAG AGGTTTCAAG ACTTTACATC CTAAGGTAAG ATATATAGCA  
 801 ATCCCCTAAA AAAAAAAAAA AAAAAAAAAA AAACCAACAA CTACATCGTA  
 851 ATCCTAAGCA AGTTAGGGTT AACTATATGA ATCATCACTA GACGGATCC

pS218 (SEQ ID NO:12)

1 AAGCTTAACT TTAATCAGAT TGCTTTCTTT AGGGAAGCGT CTTCTTAAAT  
 51 GACCATCCTC TAAATTTCTC ATGAATCTTC TTCTGTTGTC CACTCTGTTA  
 101 TCGCTGAAAC GAAATCTGAA ATTGTCATGA TGCTGACTAT TATCCAATCA  
 151 CTCAGTCTCT AATTCATATT TAGATTATCT TGTTCAACAG CCCATACTGA  
 201 TTTTTATTGT TTTGGGGTCT AACTTTTCCT TCCGGTAGTC GGTGGAGTCT  
 251 ATGAACCTAT TTCTTGAAAT GAGGATATGA CTTTATGGCC TATACTCTTT  
 301 TGGTGTCTCA AGGCCTGTCA CCTCTCATCT TTTCCTTCAA TTGACTATAG  
 351 ACTCTGTAAT ACTGTCATCT TTGGGATCTA CCGTTGTCCT CCATGTATCA  
 401 TATCTTACTC ATAATGCTTC ATTAATCTAT TTCTTATTTT CCGCTAACAT  
 451 TTATGTCTAT CACTTTATTC TGAAAACCTG AACAAGACAT TCTTTTCGTT  
 501 TTAGATCCCC TTTGCTCCAT CCAGTGGTTC TTCGGGGGAC TTAACGTTCT  
 551 CGCTCTCCTA GGGAGGCGAG CCACACTAAG GTAATATTTA TCCCTTCTAG  
 601 GCTTTCCGTG CCTATCTTCT GAGATATTTT TTTCATGCTA ATATTCACAT  
 651 CTAATTGTAA TTTTCTAGAG TGCGCCATCT GGGTGCCTCA CAAGAAGAGC  
 701 TATTAGCATC TTTGTAATAT CCTTCGGAAA TGTCAACTAA CACAACACAA  
 751 TCCATTACAC ATTTTGGGTT ACTCTAACCT CAGTCGGATA CTAATATCCT  
 801 GTCATTTTAT TAACTACAC ATGTTAGCCC CCAATAGGAT ATAACTAAGA  
 851 TGGGTGTGGC CAATTCTACA TACATCTGTT ACTGTTGAAA GTAAGTCGCA  
 901 ATGCTTTTAT TTTTCTGCCG GAGTTGAAAA TACCGATAAT CTATATTAAC  
 951 TGGGTACCTC GTACCCTTCT CATCTTTCTC CTTTACTTGT TTGAAGCTT

FIG. 3. (continued)

pS220-1 (SEQ ID NO:13)

1 AAGCTTGAAA AAGAAGAATT AAGGCTTGCT TTCTTAATTT TTAAAAATA  
 51 AAAATTATTT TGAACATCT ATACTATATT AAAAGCACGA AAACCCTATC  
 101 GAAATGTCGT TCGCCTTTTT TACCCTTTAA AAATAATTTT ACATTAGACA  
 151 AAATAGTCAT TTTACTATTT TTCCTAATAT ATAGGATTTT AAAATTAATT  
 201 TAACTTTGGC TATTAAACAT TTTCTTATAA CTTGAAATAT GTAAACTCC  
 251 TAATATTTAG AAATTTAATT AACATAACCA AGGATTTTTA TATCGGTAAT  
 301 AACTCTAATA TGGTATCCAA ATCAGTCTAG AACTCTCTTA CCTCTAATA  
 351 GTAAAGTAC TTCTAATAAA TTCATATACT TTTTCTCTCT TCTCCGATCT  
 401 CTCTTTGCTC TTCTTTTTAT GTATCCTTTC CTTTCTAATA GCCTTTTATG  
 451 AGAAGTAAAC TTTTAGGGTT GGCCCCCCT CCCCCACAA TTATATAGTT  
 501 TCTTACTCAG TTGTTGGAAT ATAATTCAA TTCTTAAATA ATTGACGGTG  
 551 ACATTGAGTT TACTTTGTG GAAGAGAATT AGATTCTCGT GTTAGTAAAA  
 601 TCGGTTAGTA ATTGATGATG CATTATTTTT ACTCTATAAT AGAGATGCAA  
 651 TTTTATTTTT GCATTTTGGG ATCAAATTGT AATGCAGTCA TATATTGATT  
 701 TCATAAATGT TTGGGATATT GTTGGTTATT TAACTAGAAA TAGACTTCTT  
 751 ATTTCATATT TATTGTTAAA ATCCTTTATT GGAGATGAAT TATTTGTTCA  
 801 CCGATTAGAA GTTGATAGTC GCTTTTGTG TAGAAGAAAT TTTACCGTAG  
 851 ACCAAGTTAA GGAGTTTTAG AAGCACTTG CATGGGAGCA TTAGTGTATG  
 901 TTATGGCTTT ATCAAATATA GGTTTTGAAG ATTCAGAGAG CCAAGAAAAG  
 951 CTAGAACCCA AGAAGTAGGA AGTTAGAGTA ATTCACAATA CCATAACGTG  
 1001 ATATAAACT TTTTATTGTA ACTCAAATCG GTAATATTTT TTGCTTTAGT  
 1051 CTTAATCGAT AAATTATTTT TTTATATTGA TTAGTTATAG GAGGCTCACA  
 1101 AAGTTGGGAA TAATTAATA ATCATATTTT GTATTTGAAC AATTTATGAA  
 1151 ATAGTAATTG GTAAAAATC ACTTTAAATT TTTATCCTAT ATCCAGAAGG  
 1201 ATTATGGTGT CTGGCATAGT TGTTTGAAG ATTTGAATCA GGGTAAAAGT  
 1251 ATGTTGTAAT TTTTATTTG TTATAGGCAT TTTTGTGCT TGATTGTTTT  
 1301 GTTGTCATTA TATTTTATTA TTTGGAAGTG TATATATATG TTTGATTAAA  
 1351 ATATAGATAA TCAATTTTAT AAGAAATTG CAACAATTAC ACAAGGATAA  
 1401 AGTCTACAAT ATGCGAGTAA AATTTGATTG AACCTAGGAT GTCATATTTA  
 1451 ATGCATATTT TATTCAATG TGTTTATTAT ACATCTATTG TATTATATG

FIG. 3. (continued)

CLONE    %AT    BINDING  
 \_\_\_\_\_ STRENGTH

GRAPHIC  
 REPRESENTATION

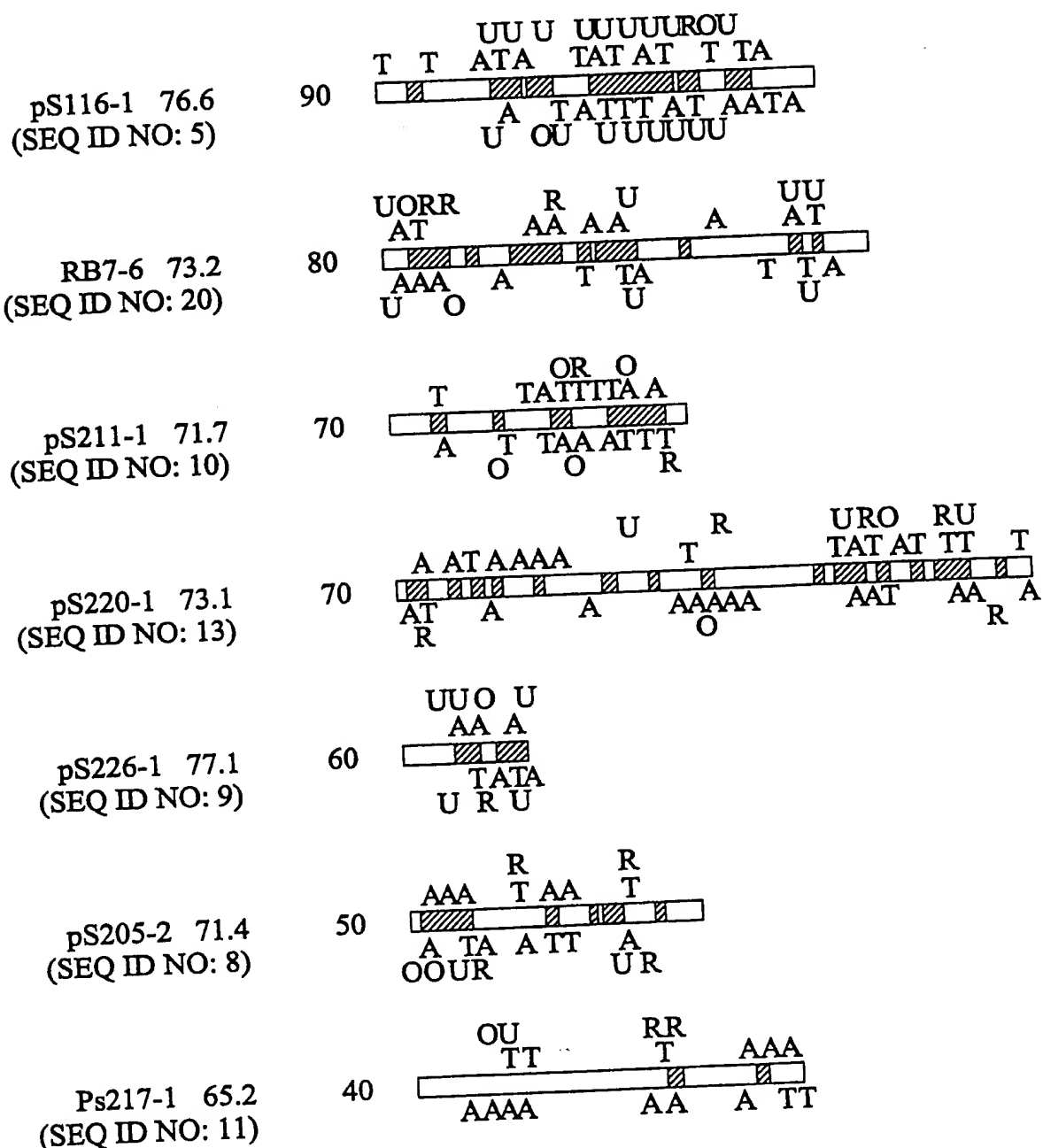


FIG. 4.

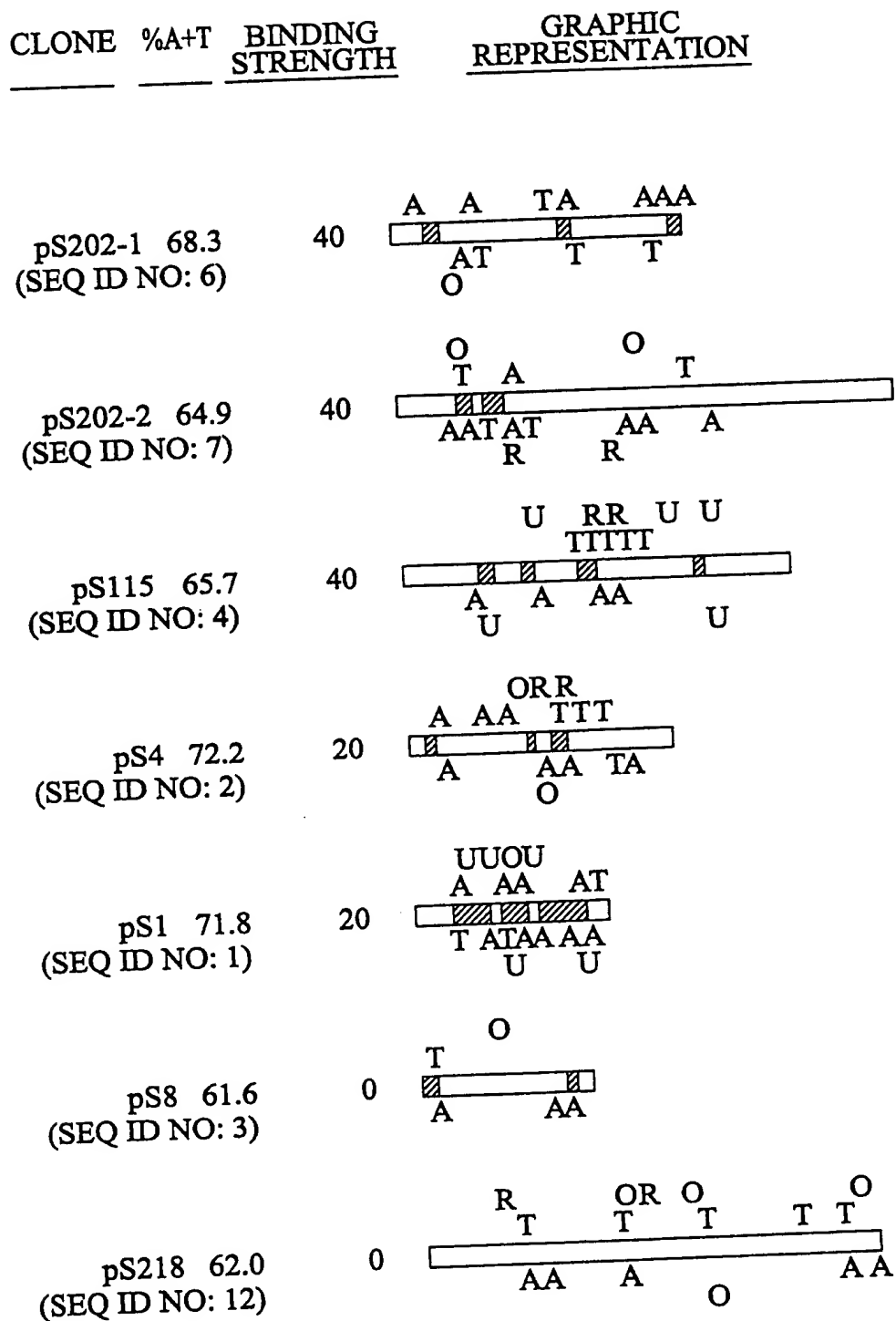
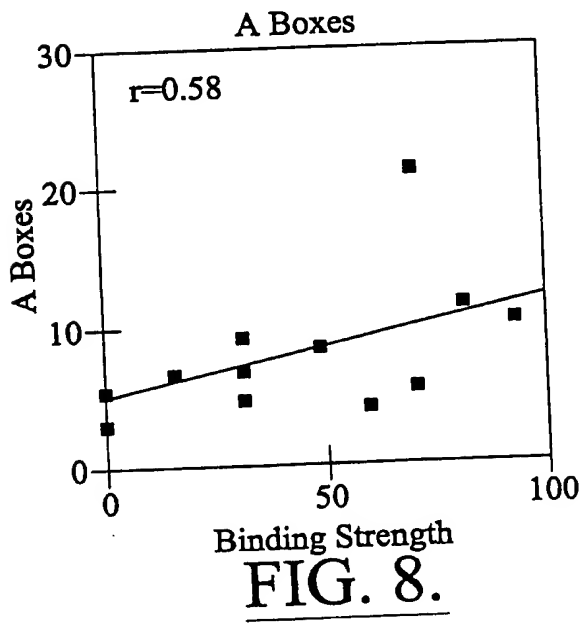
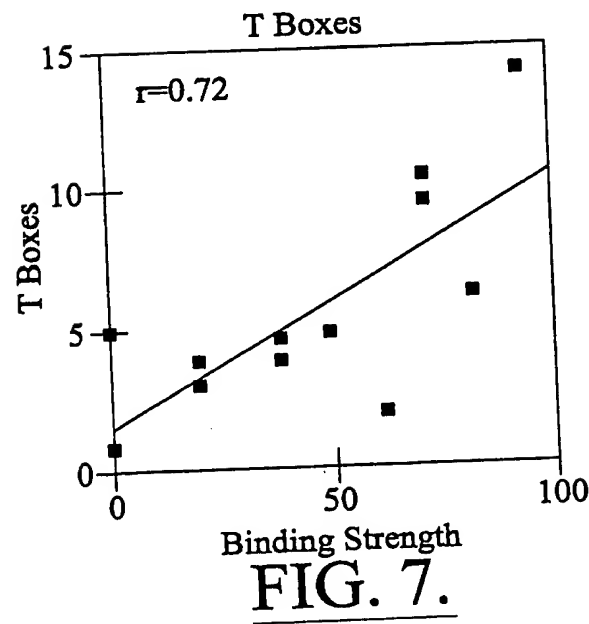
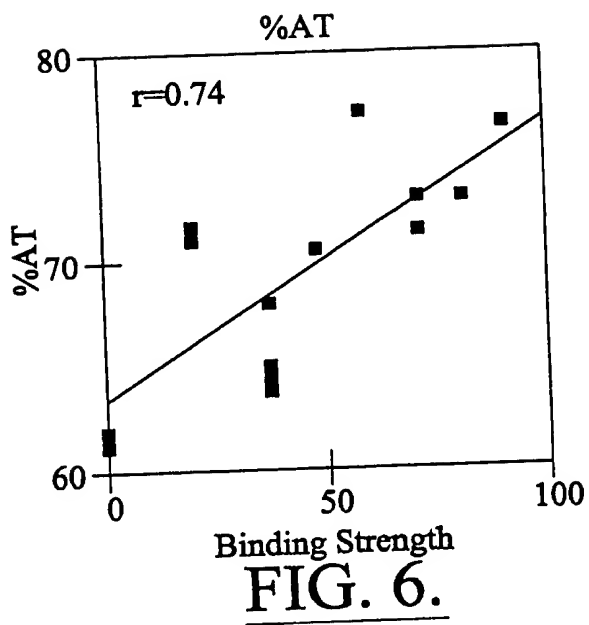
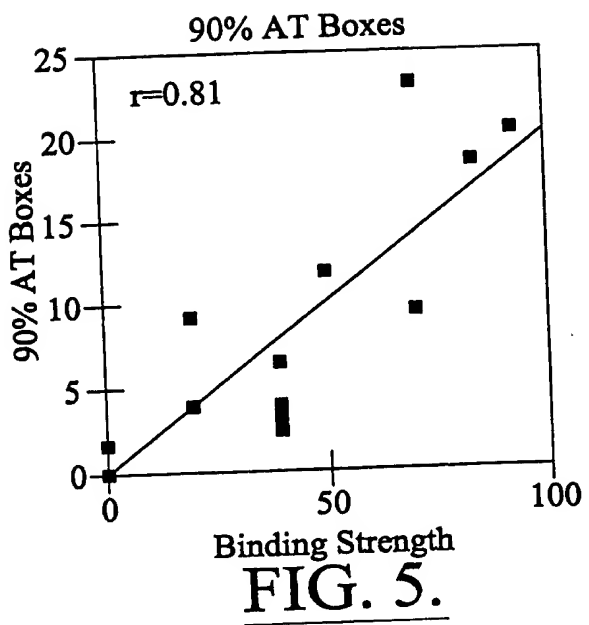


FIG. 4A.



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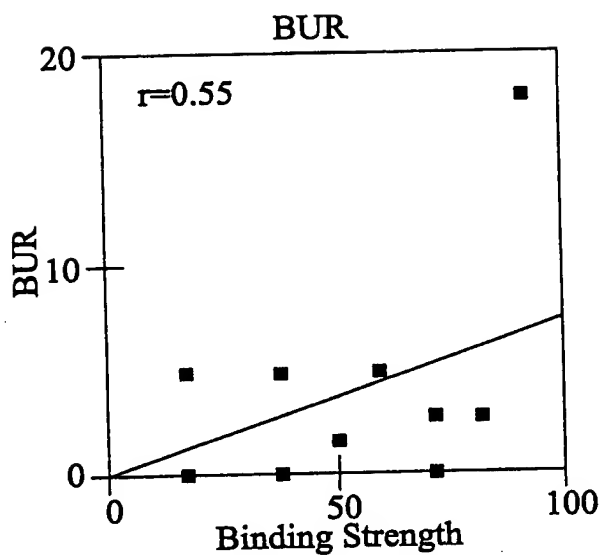


FIG. 9.

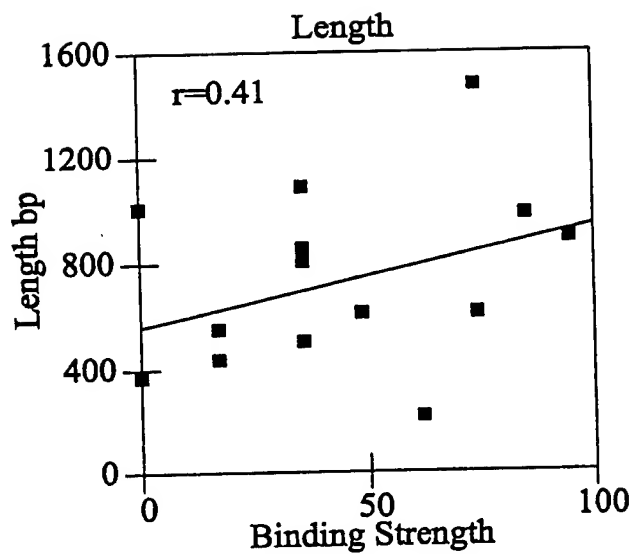


FIG. 10.

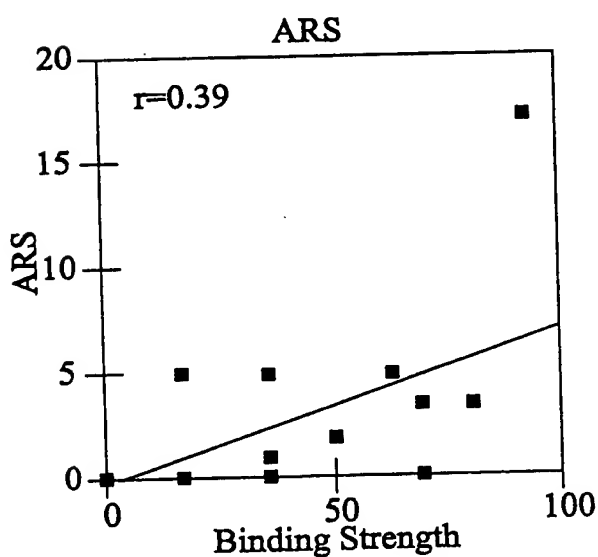


FIG. 11.

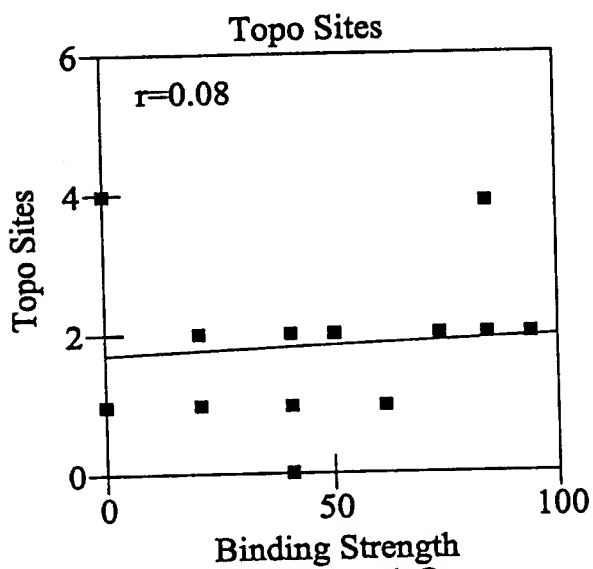


FIG. 12.